



SEQUENCE LISTING

<110> Scott, Fred W.

<120> Recombinant Multivalent Viral Vaccine

<130> 18617.0016

<140> US 09/873,881

<141> 2001-06-04

<150> US 08/552,369

<151> 1995-11-03

<160> 19

<210> 1

<211> 2254

<212> DNA

<213> feline panleukopenia virus

<220>

<223>

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aga	aat	gaa	aga	gct	aca	gga	tct	ggg	aac	ggg	tct	gga	ggc	ggg	90
Arg	Asn	Glu	Arg	Ala	Thr	Gly	Ser	Gly	Asn	Gly	Ser	Gly	Gly	Gly	
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ggt	ggt	ggt	tct	ggg	ggt	gtg	ggg	att	tct	acg	ggt	act	ttc	135
Gly	Gly	Gly	Ser	Gly	Gly	Val	Gly	Ile	Ser	Thr	Gly	Thr	Phe	
					35			40				45		

aat	aat	cag	acg	gaa	ttt	aaa	ttt	ttg	gaa	aac	gga	tgg	gtg	gaa	180
Asn	Asn	Gln	Thr	Glu	Phe	Lys	Phe	Leu	Glu	Asn	Gly	Trp	Val	Glu	
					50				55			60			

atc	aca	gca	aac	tca	agc	aga	ctt	gta	cat	tta	aat	atg	cca	gaa	225
Ile	Thr	Ala	Asn	Ser	Ser	Arg	Leu	Val	His	Leu	Asn	Met	Pro	Glu	
					65			70				75			

agt	gaa	aat	tat	aaa	aga	gta	gtt	gta	aat	aat	atg	gat	aaa	act	270
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Ser	Glu	Asn	Tyr	Lys	Arg	Val	Val	Val	Asn	Asn	Met	Asp	Lys	Thr	
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gca	gtt	aaa	gga	aac	atg	gct	tta	gat	gac	act	cat	gta	caa	att	315
Ala	Val	Lys	Gly	Asn	Met	Ala	Leu	Asp	Asp	Thr	His	Val	Gln	Ile	

95	100	105	
gta aca cct tgg tca ttg gat gca aat gct tgg gga gtt tgg Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp 110	115	120	360
ttt aat cca gga gat tgg caa cta att gtt aat act atg agt gag Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser Glu 125	130	135	405
ttg cat tta gtt agt ttt gaa caa gaa att ttt aat gtt gtt tta Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val Val Leu 140	145	150	450
aag act gtt tca gaa tct gct act cag cca cca act aaa gtt tat Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr 155	160	165	495
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aat act atg cca ttt act cca gca gct atg'aga tct gag aca ttg Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu 185	190	195	585
ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg aga tat Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr 200	205	210	630
tat ttt caa tgg gat aga aca tta ata cca tct cat act gga act Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr 215	220	225	675
agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp 230	235	240	720
gtt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu 245	250	255	765
aga aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys 260	265	270	810
aaa cca tgt aga cta aca cat aca tgg caa aca aac aga gca ttg Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu 275	280	285	855
ggc tta cca cca ttt cta aat tct ttg cct caa tct gaa gga gct			900

Gly	Leu	Pro	Pro	Phe	Leu	Asn	Ser	Leu	Pro	Gln	Ser	Glu	Gly	Ala	
290									295					300	
act	aac	ttt	ggt	gat	ata	gga	gtt	caa	caa	gat	aaa	aga	cgt	ggt	945
Thr	Asn	Phe	Gly	Asp	Ile	Gly	Val	Gln	Gln	Asp	Lys	Arg	Arg	Gly	
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gta	act	caa	atg	gga	aat	aca	gac	tat	att	act	gaa	gct	act	att	990
Val	Thr	Gln	Met	Gly	Asn	Thr	Asp	Tyr	Ile	Thr	Glu	Ala	Thr	Ile	
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Met	Arg	Pro	Ala	Glu	Val	Gly	Tyr	Ser	Ala	Pro	Tyr	Tyr	Ser	Phe	
					335				340				345		
gaa	gcg	tct	aca	caa	ggg	cca	ttt	aaa	ata	cct	att	gca	gca	gga	1080
Glu	Ala	Ser	Thr	Gln	Gly	Pro	Phe	Lys	Ile	Pro	Ile	Ala	Ala	Gly	
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cgg	ggg	gga	gcf	caa	aca	gat	gaa	aat	caa	gca	gca	gat	ggt	gat	1125
Arg	Gly	Gly	Ala	Gln	Thr	Asp	Glu	Asn	Gln	Ala	Ala	Asp	Gly	Asp	
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cca	aga	tat	gca	ttt	ggt	aga	caa	cat	ggt	caa	aaa	act	act	aca	1170
Pro	Arg	Tyr	Ala	Phe	Gly	Arg	Gln	His	Gly	Gln	Lys	Thr	Thr	Thr	
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aca	gga	gaa	aca	cct	gag	aga	ttt	aca	tat	ata	gca	cat	caa	gat	1215
Thr	Gly	Glu	Thr	Pro	Glu	Arg	Phe	Thr	Tyr	Ile	Ala	His	Gln	Asp	
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aca	gga	aga	tat	cca	gca	gga	gat	tgg	att	caa	aat	att	aac	ttt	1260
Thr	Gly	Arg	Tyr	Pro	Ala	Gly	Asp	Trp	Ile	Gln	Asn	Ile	Asn	Phe	
					410				415				420		
aac	ctt	cct	gta	aca	aat	gat	aat	gta	ttg	cta	cca	aca	gat	cca	1305
Asn	Leu	Pro	Val	Thr	Asn	Asp	Asn	Val	Leu	Leu	Pro	Thr	Asp	Pro	
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att	gga	ggt	aaa	aca	gga	atc	aac	tat	act	aat	ata	ttt	aat	act	1350
Ile	Gly	Gly	Lys	Thr	Gly	Ile	Asn	Tyr	Thr	Asn	Ile	Phe	Asn	Thr	
					440				445				450		
tat	ggt	cct	tta	act	gca	tta	aat	aat	gta	cca	cca	gtt	tat	cca	1395
Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr	Pro	
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aat	ggt	caa	att	tgg	gat	aaa	gaa	ttt	gat	act	gac	tta	aaa	cca	1440
Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe	Asp	Thr	Asp	Leu	Lys	Pro	
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aga ctt cat gta aat gca cca ttt gtt tgt caa aat aat tgt cct	1485
Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro	
485	490
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ggt caa tta ttt gta aaa gtt gcg cct aat tta aca aat gaa tat	1530
Gly Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr	
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gat cct gat gca tct gct aat atg tca aga att gta act tac tca	1575
Asp Pro Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser	
515	520
525	
gat ttt tgg tgg aaa ggt aaa tta gta ttt aaa gct aaa cta aga	1620
Asp Phe Trp Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg	
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540	
gca tct cat act tgg aat cca att caa caa atg agt att aat gta	1665
Ala Ser His Thr Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val	
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gat aac caa ttt aac tat cta cca aat aat att gga gct atg aaa	1710
Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys	
560	565
570	
att gta tat gaa aaa tct caa cta gca cct aga aaa tta tat	1752
Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr	
575	580
taatatactt actatgtttt tatggattt acatatcaac tagcacctag	1802
aaaattata taatatactt actatgtttt tatgtttt acatattatt	1852
ttaagattaa tttaattaca acatagaaat attgtacttg tatttgat	1902
aggattna aggtttgtta tatggatatac aataactgta agaaatagaa	1952
gaacatttag atcatggta gtatggata caataactgt aagaaataga	2002
agaacattta gatcatggtt agtagttgt ttataaaat gtaattgtaa	2052
actattaatg tatgttgtt tgggtgggt ggttgggttgg tttgccctta	2102
gaatatgtta aggacaaaa aaatcaataa aagacattta aaacttaatg	2152
gtctcgata ctgtctataa ggtgaactaa ccttaccata agtataact	2202
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cca ttg tgt ttt ggg aaa ttc cct att tac acg ata cta gac		84
Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp		
15 20 25		
aag ctt ggt ccc tgg agc ccg att gac ata cat cac ctc agc		126
Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser		
30 35 40		
tgc cca aac aat ttg gta gtg gag gac gaa gga tgc acc aac		168
Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn		
45 50 55		
ctg tca ggg ttc tcc tac atg gaa ctt aaa gtt gga tac atc		210
Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile		
60 65 70		
tta gcc ata aaa atg aac ggg ttc act tgc aca ggc gtt gtg		252
Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val		
75 80		
acg gag gct gaa acc tac act aac ttc gtt ggt tat gtc aca		294
Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr		
85 90 95		
acc acg ttc aaa aga aag cat ttc cgc cca aca cca gat gca		336
Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala		
100 105 110		
tgt aga gcc gcg tac aac tgg aag atg gcc ggt gac ccc aga		378
Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg		
115 120 125		
tat gaa gag tct cta cac aat ccg tac cct gac tac cgc tgg		420
Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp		
130 135 140		
ctt cga act gta aaa acc acc aag gag tct ctc gtt atc ata		462

Leu	Arg	Thr	Val	Lys	Thr	Thr	Lys	Glu	Ser	Leu	Val	Ile	Ile		
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Ser	Pro	Ser	Val	Ala	Asp	Leu	Asp	Pro	Tyr	Asp	Arg	Ser	Leu		
155					160					165					
cac	tcg	agg	gtc	tcc	cct	agc	ggg	aag	tgc	tca	gga	gta	gcg		546
His	Ser	Arg	Val	Phe	Pro	Ser	Gly	Lys	Cys	Ser	Gly	Val	Ala		
170						175					180				
gtg	tct	tct	acc	tac	tgc	tcc	act	aac	cac	gat	tac	acc	att		588
Val	Ser	Ser	Thr	Tyr	Cys	Ser	Thr	Asn	His	Asp	Tyr	Thr	Ile		
185						190					195				
tgg	atg	ccc	gag	aat	ccg	aga	cta	ggg	atg	tct	tgt	gac	att		630
Trp	Met	Pro	Glu	Asn	Pro	Arg	Leu	Gly	Met	Ser	Cys	Asp	Ile		
					200				205			210			
ttt	acc	aat	agt	aga	ggg	aag	aga	gca	tcc	aaa	ggg	agt	gag		672
Phe	Thr	Asn	Ser	Arg	Gly	Lys	Arg	Ala	Ser	Lys	Gly	Ser	Glu		
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act	tgc	ggc	ttt	gta	gat	gaa	aga	ggc	cta	tat	aag	tct	tta		714
Thr	Cys	Gly	Phe	Val	Asp	Glu	Arg	Gly	Leu	Tyr	Lys	Ser	Ile		
225					230				235						
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Lys	Gly	Ala	Cys	Lys	Leu	Lys	Leu	Cys	Gly	Val	Leu	Gly	Leu		
240						245					250				
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Arg	Leu	Met	Asp	Gly	Thr	Trp	Val	Ala	Met	Gln	Thr	Ser	Asn		
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gaa	acc	aaa	tgg	tgc	gct	ccc	gat	cag	ttg	gtg	aac	ctg	cac		840
Glu	Thr	Lys	Trp	Cys	Pro	Pro	Asp	Gln	Leu	Val	Asn	Leu	His		
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Asp	Phe	Arg	Ser	Asp	Glu	Ile	Glu	His	Leu	Val	Val	Glu	Glu		
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Leu	Val	Arg	Lys	Arg	Glu	Glu	Cys	Leu	Asp	Ala	Leu	Glu	Ser		
295						300				305					
atc	atg	aca	aac	aag	tca	gtg	agt	ttc	aga	cgt	ctc	agt	cat		966
Ile	Met	Thr	Thr	Lys	Ser	Val	Ser	Phe	Arg	Arg	Leu	Ser	His		
						310		315			320				

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ttc aac aag acc ttg atg gaa gcc gat gct cac tac aag tca Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser 340	345	350	1050
gtc aga act tgg aat gag atc ctc cct tca aaa ggg tgt tta Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu 355	360		1092
aga gtt ggg ggg agg tgt cat cct cat gtg aac ggg gtg ttt Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe 365	370	375	1134
ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile 380	385	390	1176
cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu 395	400	405	1218
ttg gaa tcc tcg gtt atc ccc ctt gtg cac ccc ctg gca gac Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp 410	415	420	1260
ccg tct acc gtt ttc aag gac ggt gac gag gct gag gat ttt Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe 425	430		1302
gtt gaa gtt cac ctt ccc gat gtg cac aat cag gtc tca gga Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly 435	440	445	1344
gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu 450	455	460	1386
agt gca ggg gcc ctg act gcc ttg atg ttg ata att ttc ctg Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu 465	470	475	1428
atg aca tgt tgt aga aga gtc aat cga tca gaa cct acg caa Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln 480	485	490	1470
cac aat ctc aga ggg aca ggg agg gag gtg tca gtc act ccc His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro			1512

495

500

caa agc ggg aag atc ata tct tca tgg gaa tca cac aag agt 1554
Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser
505 510 515

ggg ggt gag acc aga ctg tga 1575
Gly Gly Glu Thr Arg Leu
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<210> 3
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<212> DNA
<213> P11 late promoter and leader sequence

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taaaaatata gtagaatttc attttgttt tttctatgct ataa 44

<210> 4
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<212> DNA
<213> artificial sequence

<220>
<223> forward primer

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cgggatccat tttccttcg tttgccat 28

<210> 5
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<223> reverse primer

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cggttaccga tttctccgtg ataggtat 28

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<223> sequencing primer

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ctacttgcat agataggt 18

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cct cac atc aaa ttg gta atc aac ccc aac aaa ttt cta cat gtt      90
Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val
20          25          30

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ggc ttc tgc gat aac cct tta atg tgt tgt tat cct gaa tta ctal 135
Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu
35 40 45

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cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa    180
Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln
      50          55          60

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gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act 225
Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr
65 70 75

cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa 270
His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu
80 85 90

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gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac 315
Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His
95          100          105

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ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt 360
 Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu
 110 115 120

ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag 405

Phe	Arg	Leu	Glu	Ala	Asp	Asp	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Gln	
				125					130				135		
gga	aca	atg	gtt	ggg	gga	gtc	att	gct	gag	ccc	aac	gcc	caa	atg	450
Gly	Thr	Met	Val	Gly	Gly	Val	Ile	Ala	Glu	Pro	Asn	Ala	Gln	Met	
				140					145				150		
tca	acc	gca	gct	gac	atg	gcc	act	ggg	aaa	agt	gtg	gac	tct	gag	495
Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu	
				155					160				165		
tgg	gaa	gcc	ttc	ttc	tcc	ttt	cac	act	agt	gtg	aac	tgg	agc	aca	540
Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr	
				170					175				180		
tct	gaa	act	cag	ggg	aag	ata	ctc	ttt	aaa	c _{aa}	tcc	tta	gga	cca	585
Ser	Glu	Thr	Gln	Gly	Lys	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro	
				185					190				195		
ttg	ctc	aac	ccc	tac	ctt	acc	cat	ctt	gca	aag	ctg	tat	gtt	gct	630
Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala	
				200					205				210		
tgg	tct	ggt	tct	gtt	gat	gtt	agg	ttt	tct	att	tct	gga	tct	ggt	675
Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly	
				215					220				225		
gtc	ttt	gga	ggg	aaa	tta	gct	gct	att	gtt	gtg	cc _g	cca	gga	att	720
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile	
				230					235				240		
gat	cct	gtt	caa	agt	act	tca	atg	ctg	caa	tat	cct	cat	gtc	ctc	765
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu	
				245					250				255		
ttt	gat	gct	cgt	caa	gtt	gaa	cct	gtt	atc	ttt	tcc	att	ccc	gat	810
Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp	
				260					265				270		
cta	aga	agc	acc	tta	tat	cac	ctt	atg	tct	gac	act	gat	acc	aca	855
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr	
				275					280				285		
tcg	ttg	gta	atc	atg	gtg	tac	aat	gat	ctt	att	aac	ccc	tat	gct	900
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala	
				290					295				300		
aat	gac	tca	aac	tct	tcg	ggc	tgc	att	gtc	act	gtg	gaa	act	aaa	945
Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys	
				305					310				315		

ccg ggg cca gat ttc aag ttt cac ctc tta aaa cct cct ggg tct	990	
Pro Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser		
320	325	330
atg tta act cac gga tct atc cca tct gat cta atc cca aaa tca	1035	
Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser		
335	340	345
tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat	1080	
Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp		
350	355	360
ttt gta att cgg cct ttt gtg ttc cag gca aat cga cac ttt gat	1125	
Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp		
365	370	375
ttc aac caa gag aca gca ggt tgg agc acc cca agg ttt cgc cca	1170	
Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro		
380	385	390
att act atc act atc agt gtt aag gag tca gca aag ctt ggt att	1215	
Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile		
395	400	405
gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg	1260	
Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp		
410	415	420
ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat	1305	
Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr		
425	430	435
gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag	1350	
Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln		
440	445	450
tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc	1395	
Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly		
455	460	465
atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag	1440	
Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys		
470	475	480
att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc	1485	
Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala		
485	490	495
aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta	1530	
Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val		
500	505	510

ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac		1575
Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp		
515	520	525
aca ttg gcc ctg ctt ggt tat act ggt att ggt gag gaa gca att		1620
Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile		
530	535	540
ggc gct gac cgc gat aga gtt gtg cga att agc gtc ctc ccg gaa		1665
Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu		
545	550	555
cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct		1710
Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser		
560	565	570
atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct		1755
Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser		
575	580	585
caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta		1800
Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu		
590	595	600
ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat		1845
Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn		
605	610	615
gga tcc tgg ttt gac ata ggc att gat aat gat gga ttt tct ttt		1890
Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe		
620	625	630
gtt ggt gta tca agt att ggt aaa tta gag ttt cct tta act gcc		1935
Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala		
635	640	645
tcc tac atg gga att caa ttg gca aaa att cga ctt gcc tct aac		1980
Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn		
650	655	660
att agg agt gtg atg aca aaa tta tga		2007
Ile Arg Ser Val Met Thr Lys Leu		
665		

<210> 8
 <211> 582
 <212> DNA
 <213> artificial sequence

<220>

<223> hemagglutinin left arm

<400> 8

attaaacgca aatatccatg	gaaaacgcgc	agtatacaga	cgattttta	50
cagtatttgg agagtttat	aggaagtata	tagagtagaa	ccagaatttt	100
gtaaaaataa atcacattt	tatactaata	tgaaacaact	atcgatagtt	150
atattgctac tatcgatagt	atatacaacc	aaacctcatc	ctacacagat	200
atcaaaaaaa ctaggcgatg	atgctactct	atcggtaat	agaaaacaata	250
cacatggata tcttgtcatg	agttcttgg	ataagaaacc	agactccatt	300
attctcttag cagccaaaaa	cgtatgtcgta	tactttgatg	attatacagc	350
ggataaaagta tcatacgatt	caccgtatga	tactctagct	acaattatta	400
caattaaatc attgacatct	gcagatgcag	gtacttatat	atgcgcattc	450
tttataacat caacaaatga	tacggataaa	atagattatg	aagaatactt	500
catagatttgc ttgttaatc	cagctaattgt	atccactatt	gacgcgatc	550
tatcaggatc taatttctcc	gtgataggt	tc		582

<210> 9

<211> 447

<212> DNA

<213> artificial sequence

<220>

<223> hemagglutinin right arm

<400> 9

ctcttagcgcc taaccccagg	cgaccgacga	caacctttat	gatacatata	50
atgaaccaat atctgtatca	tcctcgatac	caacaacggt	agaaaagtgtt	100
acaatatcta ctacaaaata	tacaactagt	gactttata	agatattttgg	150
cattgttca ctaattttat	tattggccgt	ggcgattttc	tgtatttat	200
tatttctgt	gtggacggc	tcgtaaacaa	gaaacaaata	250
ttaactcag ataaatgtct	ggaataatta	aatctatcg	tttgagcgga	300
ccatctggtt ccggcaagac	agctatagtc	aggagactct	tacaagatta	350
tggaaatata tttggatttg	tggtatccca	taccactaga	tttcctcg	400
ctatggaacg agaagggtgtc	gactaccatt	acgttaacag	agaggcc	
				447

<210> 10

<211> 40

<212> DNA

<213> artificial sequence

<220>

<223> primer P3

<400> 10

gatacctatc acggagaaat tagatcctga tagaatcg 40

<210> 11

<211> 22

<212> DNA
<213> artificial sequence

<220>
<223> primer P1

<400> 11
attaaacgca aatatccatg gg 22

<210> 12
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> primer F2

<400> 12
gcggtaaccct ggggttaggc gatagag 27

<210> 13
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer P5

<400> 13
atttctccgt gataggtatc 20

<210> 14
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer P5

<400> 14
ggcctctctg ttaacgtaat gg 22

<210> 15
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer P2

<400> 15
gcgtcgaagt ttgagcatgt gc 22

<210> 16
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> primer P4

<400> 16
ctctagcgcc taaccccagg cgaccgacga caacctttat 40

<210> 17
<211> 840
<212> DNA
<213> feline infectious peritonitis virus

<220>
<223>

<400> 17
aaaccaaggc atataatccc gacgaagcat tttgggttg aactaaacaa a 51
atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96
Met Lys Tyr Ile Leu Ile Leu Ala Cys Ile Ile Ala Cys Val
1 5 10 15
tat ggt gaa cgc tac tgt gcc atg caa gac agt ggc ttg cag tgt 141
Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys
20 25 30
att aat ggc aca aat tca aga tgt caa acc tgc ttt gaa cgt ggt 186
Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly
35 40 45
gat ctt att tgg cat ctt gct aac tgg aac ttc agc tgg tct gta 231
Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val
50 55 60
ata ttg att gtt ttt ata aca gtg tta caa tat ggc aga cca caa 276
Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln
65 70 75

ttt agc tgg ctc gtt tat ggc att aaa atg ctg atc atg tgg cta		321
Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu		
80	85	90
tta tgg cct att gtt cta gcg ctt acg att ttt aat gca tac tct		366
Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser		
95	100	105
gag tac caa gtt tcc aga tat gta atg ttc ggc ttt agt gtt gca		411
Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala		
110	115	120
ggt gca gtt gta acg ttt gca ctt tgg atg atg tat ttt gtg aga		456
Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg		
125	130	135
tct gtt cag cta tat aga aga acc aaa tca tgg tgg tct ttt aat		501
Ser Val Gln Leu Tyr Arg Arg Thr Lys Ser Trp Trp Ser Phe Asn		
140	145	150
cct gag act aat gca att ctt tgt gtt aat gca ttg ggt aga agt		546
Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser		
155	160	165
tat gtg ctt ccc tta gat ggt act cct aca ggt gtt acc ctt act		591
Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr		
170	175	180
cta ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt		636
Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly		
185	190	195
ggt tta acc atc gag cat ttg cct aaa tac gtc atg att gct aca		681
Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr		
200	205	210
cct agt aga acc atc gtt tat aca tta gtt gga aaa caa tta aaa		726
Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys		
215	220	225
gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct		771
Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala		
230	235	240
ggt gat tac tca aca gaa gca cgt act gac aat ttg agt gaa cat		816
Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His		
245	250	255
gaa aaa tta tta cat atg gtg taa		840
Glu Lys Leu Leu His Met Val		
260		

<210> 18
 <211> 1144
 <212> DNA
 <213> feline infectious peritonitis virus

 <220>
 <223>

 <400> 18

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Met	Ala	Thr	Gln	Gly	Gln	Arg	Val	Asn	Trp	Gly	Asp	Glu	Pro	Ser		
1															15	
aaa	aga	cgt	ggt	cgt	tct	aac	tct	cgt	ggt	cgg	aag	aat	aat	gat		90
Lys	Arg	Arg	Gly	Arg	Ser	Asn	Ser	Arg	Gly	Arg	Lys	Asn	Asn	Asp		
															30	
ata	cct	ttg	tca	ttc	tac	aac	ccc	att	acc	ctc	gaa	caa	gga	tct		135
Ile	Pro	Leu	Ser	Phe	Tyr	Asn	Phe	Ile	Thr	Leu	Glu	Gln	Glu	Ser		
															45	
aaa	ttt	tgg	aat	tta	tgt	ccg	aga	gac	ctt	gtt	ccc	aaa	gga	ata		180
Lys	Phe	Trp	Asn	Leu	Cys	Pro	Arg	Asp	Leu	Val	Pro	Lys	Gly	Ile		
															60	
ggt	aat	aag	gat	caa	caa	att	ggt	tat	tgg	aat	aga	cag	att	cgt		225
Gly	Asn	Lys	Asp	Gln	Gln	Ile	Gly	Tyr	Trp	Asn	Arg	Gln	Ile	Arg		
															75	
tat	cgt	att	gta	aaa	ggc	cag	cgt	aag	gaa	ctc	gct	gag	agg	tgg		270
Tyr	Arg	Ile	Val	Lys	Gly	Gln	Arg	Lys	Glu	Leu	Ala	Glu	Arg	Trp		
															90	
ttc	ttt	tac	ttc	tta	ggt	aca	gga	cct	cat	gct	gat	gct	aaa	ttc		315
Phe	Phe	Tyr	Phe	Leu	Gly	Thr	Gly	Phe	His	Ala	Asp	Ala	Lys	Phe		
															105	
aaa	gac	aag	att	gat	gga	gtc	ttc	tgg	gtt	gca	agg	gat	ggt	gcc		360
Lys	Asp	Lys	Ile	Asp	Gly	Val	Phe	Trp	Val	Ala	Arg	Asp	Gly	Ala		
															120	
atg	aac	aag	ccc	aca	acg	ctt	ggc	act	cgt	gga	acc	aat	aac	gaa		405
Met	Asn	Lys	Pro	Thr	Thr	Leu	Gly	Thr	Arg	Gly	Thr	Asn	Asn	Glu		
															135	
tcc	aaa	cca	ctg	aga	ttt	gat	ggt	aag	ata	ccg	cca	cag	ttt	cag		450
Ser	Lys	Pro	Leu	Arg	Phe	Asp	Gly	Lys	Ile	Pro	Pro	Gln	Phe	Gln		
															150	
ctt	gaa	gtg	aac	cgt	tct	agg	aac	aat	tca	agg	tct	qgt	tct	caq		495

Leu	Glu	Val	Asn	Arg	Ser	Arg	Asn	Asn	Ser	Arg	Ser	Gly	Ser	Gln	
				155					160						165
tct	aga	tct	gtt	tca	aga	aac	aga	tct	caa	tct	aga	gga	aga	cac	540
Ser	Arg	Ser	Val	Ser	Arg	Asn	Arg	Ser	Gln	Ser	Arg	Gly	Arg	His	
				170					175						180
cat	tcc	aat	aac	cag	aat	aat	aat	gtt	gag	gat	aca	att	gta	gcc	585
His	Ser	Asn	Asn	Gln	Asn	Asn	Asn	Val	Glu	Asp	Thr	Ile	Val	Ala	
				185					190						195
gtg	ctt	gaa	aaa	tta	ggt	gtt	act	gac	aaa	caa	agg	tca	cgt	tct	630
Val	Leu	Glu	Lys	Leu	Gly	Val	Thr	Asp	Lys	Gln	Arg	Ser	Arg	Ser	
				200					205						210
aaa	cct	aga	gaa	cgt	agt	gat	tcc	aaa	cct	agg	gac	aca	aca	cct	675
Lys	Pro	Arg	Glu	Arg	Ser	Asp	Ser	Lys	Pro	Arg	Asp	Thr	Thr	Pro	
				215					220						225
aag	aat	gcc	aac	aaa	cac	acc	tgg	aag	aaa	act	gca	ggc	aag	gga	720
Lys	Asn	Ala	Asn	Lys	His	Thr	Trp	Lys	Lys	Thr	Ala	Gly	Lys	Gly	
				230					235						240
gat	gtg	aca	act	ttc	tat	ggt	gct	aga	agt	agt	tca	gct	aac	ttt	765
Asp	Val	Thr	Thr	Phe	Tyr	Gly	Ala	Arg	Ser	Ser	Ser	Ala	Asn	Phe	
				245					250						255
ggt	gat	agt	gat	ctc	gtt	gcc	aat	ggt	aac	gct	gcc	aaa	tgc	tac	810
Gly	Asp	Ser	Asp	Leu	Val	Ala	Asn	Gly	Asn	Ala	Ala	Lys	Cys	Tyr	
				260					265						270
cct	cag	ata	gct	gaa	tgt	gtt	cca	tca	gtg	tct	agc	ata	atc	ttt	855
Pro	Gln	Ile	Ala	Glu	Cys	Val	Pro	Ser	Val	Ser	Ser	Ile	Ile	Phe	
				275					280						285
ggc	agt	caa	tgg	tct	gct	gaa	gct	ggt	gat	caa	gtg	aaa	gtc		900
Gly	Ser	Gln	Trp	Ser	Ala	Glu	Glu	Ala	Gly	Asp	Gln	Val	Lys	Val	
				290					295						300
acg	ctc	act	cac	acc	tac	tac	ctg	cca	aag	gat	gat	gcc	aaa	act	945
Thr	Leu	Thr	His	Thr	Tyr	Tyr	Leu	Pro	Lys	Asp	Asp	Ala	Lys	Thr	
				305					310						315
agt	caa	ttc	cta	gaa	cag	att	gac	gct	tac	aag	cga	cct	tct	gaa	990
Ser	Gln	Phe	Leu	Glu	Gln	Ile	Asp	Ala	Tyr	Lys	Atg	Pro	Ser	Glu	
				320					325						330
gtg	gct	aag	gat	cag	agg	caa	aga	aga	tcc	cgt	tct	aag	tct	gct	1035
Val	Ala	Lys	Asp	Gln	Arg	Gln	Arg	Arg	Ser	Arg	Ser	Lys	Ser	Ala	
				335					340						345

gat aag aag cct gag gag ttg tct gta act ctt gtg gag gca tac	1080
Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr	
350	355
	360
aca gat gtg ttt gat gac aca cag gtt gag atg att gat gag gtt	1125
Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val	
365	370
	375
acg aac taa acgcatgctc	1144
Thr Asn	

<210> 19
<211> 1979
<212> DNA
<213> feline leukemia virus

<220>
<223>

<400> 19		
accaccaatc aagacaccttc ggacagcccc agctcagacg atccatcaag	50	
atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc	95	
Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu		
1	5	10
		15
tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac	140	
Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp		
20	25	30
ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act	185	
Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr		
35	40	45
tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc	230	
Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr		
50	55	60
tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt	275	
Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val		
65	70	75
gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta	320	
Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu		
80	85	90
aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365	
Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys		
95	100	105

tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr 110 115 120	410
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys 125 130 135	455
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp 140 145 150	500
gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser 155 160 165	545
tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser 170 175 180	590
tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys 185 190 195	635
gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg 200 205 210	680
cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 215 220 225	725
cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn 230 235 240	770
cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr 245 250 255	815
ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala 260 265 270	860
cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cggttatttggg Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly 275 280 285	905
acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala	950

290	295	300	
tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 305	310	315	995
ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 320	325	330	1040
acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act Asn Tyr Ser Asn Gln Thr Asn Pro Pro Ser Cys Leu Ser Ile 335	340	345	1085
ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met 350	355	360	1130
tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys 365	370	375	1175
aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn 380	385	390	1220
ggc acc tat tgg gcc tgt aac act gga ctc acc cca tgc att tcc Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser 395	400	405	1265
atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu 410	415	420	1310
tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr 425	430	435	1355
cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile Ser Leu 440	445	450	1400
acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala 455	460	465	1445
gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln 470	475	480	1490
ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta			1535

Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu		
					485				490						495	
gaa	gaa	tca	att	agt	gcc	tta	gaa	aag	tcc	ctg	acc	tcc	ctt	tct		1580
Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser		
					500				505						510	
gaa	gta	gtc	tta	caa	aac	aga	cgg	ggc	cta	gat	att	cta	ttc	tta		1625
Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu		
					515				520						525	
caa	gag	gga	ggg	ctc	tgt	gcc	gca	ttg	aaa	gaa	gaa	tgt	tgc	ttc		1670
Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe		
					530				535						540	
tat	gcg	gat	cac	acc	gga	ctc	gtc	cga	gac	aat	atg	gcc	aaa	tta		1715
Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu		
					545				550						555	
aga	gaa	aga	cta	aaa	cag	cgg	caa	caa	ctg	ttt	gac	tcc	caa	cag		1760
Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln		
					560				565						570	
gga	tgg	ttt	gaa	gga	tgg	ttc	aac	aag	tcc	ccc	tgg	ttt	aca	acc		1805
Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr		
					575				580						585	
cta	att	tcc	tcc	att	atg	ggc	ccc	tta	cta	atc	cta	ctc	cta	att		1850
Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Ile			
					590				595						600	
ctc	ctc	ttc	ggc	cca	tgc	atc	ctt	aac	cga	tta	gta	caa	ttc	gta		1895
Leu	Leu	Phe	Gly	Pro	Cys	Ile	Leu	Asn	Arg	Leu	Val	Gln	Phe	Val		
					605				610						615	
aaa	gac	aga	ata	tct	gtg	gta	cag	gct	tta	att	tta	acc	caa	cag		1940
Lys	Asp	Arg	Ile	Ser	Val	Val	Gln	Ala	Leu	Ile	Leu	Thr	Gln	Gln		
					620				625						630	
tac	caa	cag	ata	aag	caa	tac	gat	ccg	gac	cga	cca	tga				1979
Tyr	Gln	Gln	Ile	Lys	Gln	Tyr	Asp	Pro	Asp	Arg	Pro					
					635				640							